


```

/bd_xref="taxon:9606"
/clone="IMAGE:3948893"
/clone_1lb="NH_McC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(5). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      203 a      259 c      257 g      143 t      1 others
ORIGIN

```

[illegible]

Db 780 TGGCCACACTAACTCCGACAAAACGTCTCCGAGAAATTTCTACCTTGAACATTAGG 839

Oy 1264 GAGAGAGCTATTTTGTGACATTGTGTTTAAAGAGACAAAACCTGAAC 1315

Db 840 GAGAGGCTTATTTGACACTGGGGCTTAAGAGACAAAATTTGACCAATTC 891

RESULT 2					
BE271316					
LOCUS	628 bp	mRNA	linear	EST 26-OCT-2000	
DEFINITION	G0114002F01 NIH_MGC_9 Homo sapiens	cDNA	clone IMAGE:3049468 5',		
ACCESION	BE271316				
VERSION	BE271316				
KEYWORDS	BE271316.1 GI:9144976				
	.EST.				

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 628)	NIH-MGC http://mgc.ncl.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
					Contact: Robert Strausberg, Ph.D.

FEATURES
 Tissue Procurement: DCTD/DTP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov
 Plate: L10CM93 row: k column: 05
 High quality sequence stop: 628.
 Location/Qualifiers

source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3049468"
/clone_lib="NH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB1; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

Query Match	39.1%	Score 614.4	DB 10	Length 628
Best Local Similarity	99.7%	Pred. No. 5.4e-74		
Matches 626	Conservative	0	Mismatches 1	Indels 1
				Gaps 1
QY	807	CCCTAGTGAGACAGACACCTTCGTGAGTACAGTCCCGATCAAGGGCAAGAGACGGAATT	866	
Db	1	CCCTAGTGAGACAGACACCTTCGTGAGTACAGTCCCGATCAAGGGCAAGAGACGGAATT	60	
QY	867	CTACCTGTGCATGAGACCGCAAGGCACCTCTGGGGGAAGCCCGATGGCACACAGCAAGA	926	
Db	61	CTACCTGTGCATGAGACCGCAAGGCACCTCTGGGGGAAGCCCGATGGCACACAGCAAGA	120	
QY	927	GTGTGTGTTTCATCGAAGAGGTTCTGGAGACACATCACGGCCCTGATGTGCGCTAACTA	986	
Db	121	GTGTGTGTTTCATCGAAGAGGTTCTGGAGACACATCACGGCCCTGATGTGCGCTAACTA	180	
QY	987	CTCCGGGCTGGTACGTGGGCTTCACCAAGAGGGGCGCGCGGAAGGGCCCCCAAGACCGG	1046	
Db	181	CTCCGGGCTGGTACGTGGGCTTCACCAAGAGGGGCGCGCGGAAGGGCCCCCAAGACCGG	240	

QY 1047 GGAGACACGAGGACGATTCATGACGCGTACCCAGGAGGAGCCGAGCTTCA 1106
 |||||||
 Db 241 GGAGACACGAGGACGATTCATGACGCGTACCCAGGAGGAGCCGAGCTTCA 300
 |||||||
 QY 1107 GAAGCCCTTCAAGTACACGAGCGGTGACCAAGAGGTCCCGTGGATCCGCGCCACACACC 1166
 |||||||
 Db 301 GAAGCCCTTCAAGTACACGAGCGGTGACCAAGAGGTCCCGTGGATCCGCGCCACACACC 360
 |||||||
 QY 1167 TGCCTAGGACACCCCGCGCGCCCTCAGTCCGCTGGCCACACTCACCAGAA 1226
 |||||||
 Db 361 TGCCTAGGACACCCCGCGCGCCCTCAGTCCGCTGGCCACACTCACCAGAA 420
 |||||||
 QY 1227 AACTGACATGAGGATATTTTACATGATAAATAGGAGAGCTCATTTTGTACAT 1286
 |||||||
 Db 421 AACTGACATGAGGATATTTTACATGATAAATAGGAGAGCTCATTTTGTACAT 480
 |||||||
 QY 1287 TGTGTTAAAGAGACAAAACCTGACCAAACTCTTGCGGAGGAGGTGATAA-GGAT 1345
 |||||||
 Db 481 TGTGTTAAAGAGACAAAACCTGACCAAACTCTTGCGGAGGAGGTGATAAAGGAT 540
 |||||||
 QY 1346 TTTATGTTGACTGAAACCCCGATGACAAAGACTCAGCAAAAGGACTGTAGTCAAC 1405
 |||||||
 Db 541 CTTATGTTGACTGAAACCCCGATGACAAAGACTCAGCAAAAGGACTGTAGTCAAC 600
 |||||||
 QY 1406 CCACAGGTGCTGTCTCTCTCTAGAAC 1433
 |||||||
 Db 601 CCACAGGTGCTGTCTCTCTCTAGAAC 628
 |||||||

RESULT 3
 BE315016 639 bp mRNA linear EST 26-OCT-2000
 LOCUS 601140772F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3049984 5,
 DEFINITION
 mRNA sequence.
 BE315016
 VERSION
 BE315016.1 GI:9145233
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 639)
 NIH-MGC http://mgs.nci.nih.gov/.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L1CM94 row: P column: 17
 High quality sequence stop: 637.
 Location/Qualifiers
 1..639
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NIH_MGC_9"
 /tissue_type="adenocarcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: ovary; Vector: pOTB; Site: 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 148 a 194 c 199 g 98 t
 ORIGIN

Query Match 39.1%; Score 613.4; DB 10; Length 639;
 Best Local Similarity 99.5%; Pred. No. 7.3e-74;
 Matches 636; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 599 TGCCTGCTTCAGTACAGTGTGCTGGCC-GAGGAGAACGTGACTTCGCATCCAC 657
 |||||||
 Db 1 TGCCTGCTTCAGTACAGTGTGCTGGCCGAGGAGAACGTGACTTCGCATCCAC 60
 |||||||
 QY 658 GTGAGAACACAGACGCGGGCTCGGAGAGATGTGACCCGTAAGACCTCGCTTACAC 717
 |||||||
 Db 61 GTGAGAACACAGACGCGGGCTCGGAGAGATGTGACCCGTAAGACCTCGCTTACAC 120
 |||||||
 QY 718 CTCTACACCCGACAGTGGGAAACACTCCAGGCTCGGGCCGAGGATGAGCCCGC 777
 |||||||
 Db 121 CTCTACACCCGACAGTGGGAAACACTCCAGGCTCGGGCCGAGGATGAGCCCGC 180
 |||||||
 QY 778 GCGCAGATGGGAGCAATGATGCCCAGCTCTAGTGAGACAGACACCTTCGTAGTCAA 837
 |||||||
 Db 181 GCGCAGATGGGAGCAATGATGCCCAGCTCTAGTGAGACAGACACCTTCGTAGTCAA 240
 |||||||
 QY 838 GTCCGATCAAGGCGCAAGAGAGGAAATTTCTACCTGTGATGAACCGCAAAAGCAAGCTC 897
 |||||||
 Db 241 GTCCGATCAAGGCGCAAGAGAGGAAATTTCTACCTGTGATGAACCGCAAAAGCAAGCTC 300
 |||||||
 QY 898 GTGGGAGAGCCCGATGGCAGCAGAGAGTGTGTTCATCGAAGAGTTCTGGAGAAC 957
 |||||||
 Db 301 GTGGGAGAGCCCGATGGCAGCAGAGAGTGTGTTCATCGAAGAGTTCTGGAGAAC 360
 |||||||
 QY 958 AACTACAGGCGCTGATGTGCTAGTACGCGCTGATGAGTGGGCTTACCAAGAA- 1016
 |||||||
 Db 361 AACTACAGGCGCTGATGTGCTAGTACGCGCTGATGAGTGGGCTTACCAAGAA- 420
 |||||||
 QY 1017 GGGGCGGCGCGGAGAGGCGCCCAAGACCCGGGAGAACGACGAGCTGATTTATGAA 1076
 |||||||
 Db 421 GGGGCGGCGCGGAGAGGCGCCCAAGACCCGGGAGAACGACGAGCTGATTTATGAA 480
 |||||||
 QY 1077 GCGCTACCCCAAGGGGCGCGGAGCTTCAAGGCTTCAAGTACAGAGGTATACAA 1136
 |||||||
 Db 481 GCGCTACCCCAAGGGGCGCGGAGCTTCAAGGCTTCAAGTACAGAGGTATACAA 540
 |||||||
 QY 1137 GAGGTCCCGTGGATCCCGGCCACACACCTGCTAGGCGCAACCCCGCGGCGCTTACG 1196
 |||||||
 Db 541 GAGGTCCCGTGGATCCCGGCCACACACCTGCTAGGCGCAACCCCGCGGCGCTTACG 600
 |||||||
 QY 1197 GTCCGCTGGCCACACTGACACTCCAGAAACTGCAATC 1235
 |||||||
 Db 601 GTCCGCTGGCCACACTGACACTCCAGAAACTGCAATC 639
 |||||||

RESULT 4
 A1743298 455 bp mRNA linear EST 20-DEC-1999
 LOCUS w911b03.x1 Soares_NSF_F8_9W_OT_PA_S1 Homo sapiens CDNA clone
 DEFINITION
 IMAGE:2372429 3', similar to TR:076093 076093 FIBROBLAST GROWTH
 FACTOR 18. ;, mRNA sequence.
 A1743298
 VERSION
 A1743298.1 GI:5111586
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 455)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 561 Std Error: 0.00

RESULT 6

Db 421 GAGGACTTGATGAGGAACCAACACTTT 449

QY 1075 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 1134
 |||||||
 Db 1 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 60
 |||||||
 QY 1135 AAGAGTCCCGTGGATCCGCGCCACACACCTTCCCTAGGCGACCCCGCGGCCCTC 1194
 |||||||
 Db 61 AAGAGTCCCGTGGATCCGCGCCACACACCTTCCCTAGGCGACCCCGCGGCCCTC 120
 |||||||
 QY 1195 AGTCCGCTGGCCACACTCACAATCCAGAAAACTCATCAGAGAAATATTTTACATG 1254
 |||||||
 Db 121 AGTCCGCTGGCCACACTCACAATCCAGAAAACTCATCAGAGAAATATTTTACATG 180
 |||||||
 QY 1255 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACTGAA 1314
 |||||||
 Db 181 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACTGAA 240
 |||||||
 QY 1315 CAAACCTCTGGGGGAGGGGGATAGAGATTTTATTTGTTGACTTGAACCCCGATGAC 1374
 |||||||
 Db 241 CAAACCTCTGGGGGAGGGGGATAGAGATTTTATTTGTTGACTTGAACCCCGATGAC 300
 |||||||
 QY 1375 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTAGAGACA 1434
 |||||||
 Db 301 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTAGAGACA 360
 |||||||
 QY 1435 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAAACAACCTTTGAGAG 1494
 |||||||
 Db 361 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAAACAACCTTTGAGAG 420
 |||||||
 QY 1495 CCAAGCTCTTTTCC 1510
 |||||||
 Db 421 CCAAGCTCTTTTCC 436
 |||||||

RESULT 8
 A1621022 427 bp mRNA linear EST 21-APR-1999
 LOCUS t576a11.x1 NCI-CGAP.GC6 Homo sapiens cDNA clone IMAGE:2237180 3'
 DEFINITION similar to TR:076093 076093 FIBROBLAST GROWTH FACTOR 18. ; mRNA
 sequence.
 ACCESSION A1621022
 VERSION A1621022.1 GI:4630148
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 427)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bcrf.org
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bcrf/image/image.html
 Seg primer: -400p from Gibco.
 Location/Qualifiers
 1. 427
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2237180"
 /clone_lib="NCI-CGAP.GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA
 from the normalized library NCI-CGAP.GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 1257096-1258631, 146964-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo.
 BASE COUNT 132 a 116 c 97 g 81 t 1 others
 ORIGIN

Query Match 27.0%; Score 424.4; DB 9; Length 427;
 Best Local Similarity 99.5%; Pred. No. 2.8e-48;
 Matches 425; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1075 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 1134
 |||||||
 Db 1 AAGCGTACCCCAAGGGGAGCCGAGCTTCAGAGCCCTTCAAGTACAGCGGTGACC 60
 |||||||
 QY 1135 AAGAGTCCCGTGGATCCGCGCCACACACCTTCCCTAGGCGACCCCGCGGCCCTC 1194
 |||||||
 Db 61 AAGAGTCCCGTGGATCCGCGCCACACACCTTCCCTAGGCGACCCCGCGGCCCTC 120
 |||||||
 QY 1195 AGTCCGCTGGCCACACTCACAATCCAGAAAACTCATCAGAGAAATATTTTACATG 1254
 |||||||
 Db 121 AGTCCGCTGGCCACACTCACAATCCAGAAAACTCATCAGAGAAATATTTTACATG 180
 |||||||
 QY 1255 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACTGAA 1314
 |||||||
 Db 181 AAAAATAGAGAGAGCTCTATTTTGTATCTGTGTTAAAGAACACAAAACTGAA 240
 |||||||
 QY 1315 CAAACCTCTGGGGGAGGGGGATAGAGATTTTATTTGTTGACTTGAACCCCGATGAC 1374
 |||||||
 Db 241 CAAACCTCTGGGGGAGGGGGATAGAGATTTTATTTGTTGACTTGAACCCCGATGAC 300
 |||||||
 QY 1375 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTAGAGACA 1434
 |||||||
 Db 301 AAAAGACTCAGCAAGAGGAGCTGATCAACCCACAGGCTTGTCTCTAGAGACA 360
 |||||||
 QY 1435 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAAACAACCTTTGAGAG 1494
 |||||||
 Db 361 GACAACTCTAACTCTGTCGCCAAGAGAGACTTGAATGAGAAAAACAACCTTTGAGAG 420
 |||||||
 QY 1495 CCAAGCT 1501
 |||||||
 Db 421 CCAAGCT 427
 |||||||

RESULT 9
 BF471928 617 bp mRNA linear EST 04-DEC-2000
 LOCUS BF471928
 DEFINITION UI-M-BH3-awr-c-01-0-UI.r1 NIH.BMAP.M.S4 Mus musculus cDNA clone
 BF471928
 ACCESSION BF471928
 VERSION BF471928.1 GI:11541111
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 617)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd., Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@nlin.nih.gov

Matches 444: Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 1075 AAGCGTACCCCAAGGGGACCGGAGCTTCAGAGACCCCTTCAAGTACACGAGGTGACC 1134
|||||
Db 1 AAGCGTACCCCAAGGGGACCGGAGCTTCAGAGACCCCTTCAAGTACACGAGGTGACC 60
|||||

QY 1135 AAGAGTCCCTCGGATCCGGCCACACACCTTGGCTTGGCCACCCCGCGGCCCTC 1194
|||||
Db 61 AAGAGTCCCTCGGATCCGGCCACACACCTTGGCTTGGCCACCCCGCGGCCCTC 120
|||||

QY 1195 AGTTCGCCCTGGCCACACTCAGTCCAGAAACCTGATCAGAGAAATTTTATACATG 1254
|||||
Db 121 AGTTCGCCCTGGCCACACTCAGTCCAGAAACCTGATCAGAGAAATTTTATACATG 180
|||||

QY 1255 AAAAATTAAGAGAAGACTCTATTTTGTGACTGTGTGTTAAAGACAAAACGAGAC 1314
|||||
Db 181 AAAAATTAAGAGAAGACTCTATTTTGTGACTGTGTGTTAAAGACAAAACGAGAC 240
|||||

QY 1315 CAAACACTCTGGGGGAGGGGTATAGATTTATTGTTGACTTGAACCCCGCA -TGA 1373
|||||
Db 241 CAAACACTCTGGGGGAGGGGTATAGATTTATTGTTGACTTGAACCCCGCATTTGA 300
|||||

QY 1374 CAAAGACTCAG -GCAAGGAGACTGTAGTCAACCCACAGGTGC -TTGTCTCTCTAGGA 1431
|||||
Db 301 CAAAGACTCAGGCAAGGAGACTGTAGTCAACCCACAGGTGCTTGTCTCTCTAGGA 360
|||||

QY 1432 ACAGACACTCTAAACCTGTCCTCCAGAGAGAGACTTGAATGAGAAACCAACTTTGAG 1491
|||||
Db 361 ACAGACACTCTAAACCTGTCCTCCAGAGAGAGACTTGAATGAGAAACCAACTTTGAG 420
|||||

QY 1492 AAGCCAAAGTCTTTTCCCAAGGTCT 1520
|||||
Db 421 AAGCCAAAGTCTTTTCCCAAGGTCT 449
|||||

RESULT 11
BF564483/c 517 bp mRNA linear EST 12-DEC-2000
LOCUS UI-R-BU0-amu-b-08-0-UI.r1 UI-R-BU0 Rattus norvegicus cDNA clone
DEFINITION UI-R-BU0-amu-b-08-0-UI.5, mRNA sequence.
ACCESSION BF564483 GI:11674213
VERSION BF564483
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 517)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE
COMMENT 97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1801316
Seq primer: M13 Forward.
Location/Qualifiers
1. 517
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BU0-amu-b-08-0-UI"
/clone_11b="UI-R-BU0"

/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7AD-pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-BU0
library is a subtracted library derived from a mixture of
eye and ganglia tissues. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratist.eng.uiowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)" 1 others
BASE COUNT 89 a 154 c 140 g 133 t
ORIGIN

Query Match 26.0%; Score 408; DB 12; Length 517;
Best Local Similarity 88.7%; Pred. No. 4.1e-46;
Matches 441; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 680 GGGACATGTGAGCCCGTAACGAGTGGGCTGTACACGCTTACAGCCGACCAATGGGA 739
|||||
Db 517 GCGATGATGTGAGTGGGACGAGTGGGCTGTACACGCTTACAGCAGACGAGCAATGGGA 458
|||||

QY 740 AACACATCCAGTCTGGGCGGAGATCAGTGCAGCGGCGAGAGATGGGACCAATG 799
|||||
Db 457 AGCAGATTCAGTCTGGGCGGAGATCAGTGCAGCGGCGAGAGATGGGACCAATG 398
|||||

QY 800 CCAAGCTCTAGTGGAGACAGACACTTGGTACTCAAGTCCGATCAAGGCAAGAGA 859
|||||
Db 397 CCAAGCTCTAGTGGAGACAGACACTTGGTACTCAAGTCCGATCAAGGCAAGAGA 338
|||||

QY 860 CGGAATCTACCTGTCATGACGACGACGACGACGACGACGACGACGACGACGAC 919
|||||
Db 337 CAGAGTTTACCTGTCATGACGACGACGACGACGACGACGACGACGACGACGAC 278
|||||

QY 920 GCAAGAGATGTGTCATGACGACGACGACGACGACGACGACGACGACGACGAC 979
|||||
Db 277 GCAAGAGATGTGTCATGACGACGACGACGACGACGACGACGACGACGACGAC 218.
|||||

QY 980 CTAAGTACTCCGGCTGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1039
|||||
Db 217 CCAAGTACTCCGGCTGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 158
|||||

QY 1040 AGACCCGGGAGACACGACGACGACGACGACGACGACGACGACGACGACGAC 1099
|||||
Db 157 AGACCCGGGAGACACGACGACGACGACGACGACGACGACGACGACGACGAC 98
|||||

QY 1100 AGCTTCAAGAGCCCTTCAAGTACACGAGCGGTGACCAAGAGTCCGCTGATCCGCCA 1159
|||||
Db 97 AGCTTCAAGAGCCCTTCAAGTACACGAGCGGTGACCAAGAGTCCGCTGATCCGCCA 38
|||||

QY 1160 CACACCTTGGCTTGGCC 1176
|||||
Db 37 CTCACCCCGCTAGGTC 21
|||||

RESULT 12
BG800960 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0081-34 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,
mRNA sequence.
ACCESSION BG800960
VERSION BG800960.1 GI:17947827
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
JOURNAL MEDLINE
21671825


```

OY 1435 GACAACTTAACCTCGTCCCGACAGAGAGACTTGATGAGGA 1476
DB 361 GACAACTTAACCTCGTCCCGACAGAGAGACTTGATGAGGA 402

RESULT 14
AI002437 401 bp mRNA linear EST 23-JUL-1998
LOCUS or78f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1601991 3',
DEFINITION mRNA sequence.
ACCESSION AI002437
VERSION AI002437.1 GI:3202771
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 841 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 394.
FEATURES
Source location/Qualifiers
1..401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1601991"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pRT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 119 a 110 c 94 g 78 t
ORIGIN
Query Match 25.4%; Score 399.4; DB 9; Length 401;
Best Local Similarity 99.8%; Pred. No. 6.8e-45;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1075 AAGCGCTACCCAGGCGGAGCGGAGCTTCAGAAAGCCCTTAAGTACGACGAGTACC 1134
DB 1 AAGCGCTACCCAGGCGGAGCGGAGCTTCAGAAAGCCCTTAAGTACGACGAGTACC 60

OY 1135 AAGAGTCCCGTCGGATCCGCGCCACACACACCTGCTAGCCACCGCGCGCGCCCTC 1194
DB 61 AAGAGTCCCGTCGGATCCGCGCCACACACACCTGCTAGCCACCGCGCGCGCCCTC 120

OY 1195 AGTGGCCCTGGCCACACTCACACTCCAGAAAGCTGATCAGAGAAATATTTTACATG 1254
DB 121 AGTGGCCCTGGCCACACTCACACTCCAGAAAGCTGATCAGAGAAATATTTTACATG 180

OY 1235 AAAAATAAGGAAGAGCTCTATTTTGTATCTTGTGTTTAAAGAGACAAAAGTGAAC 1314

```

```

DB 181 AAAAATAAGGAAGAGAGCTCTATTTTGTATCTTGTGTTTAAAGAGACAAAAGTGAAC 240
OY 1315 CAAAACTCTGGGGGGAGGGGATGATTAAGATTTTATTTGTTGACTTGAAACCCCGATGAC 1374
DB 241 CAAAACTCTGGGGGGAGGGGATGATTAAGATTTTATTTGTTGACTTGAAACCCCGATGAC 300

OY 1375 AAAAGACTCAGCCAAAGGAGACTGTACTCAACCCACAGAGTGTCTCTCTAGAGACA 1434
DB 301 AAAAGACTCAGCCAAAGGAGACTGTACTCAACCCACAGAGTGTCTCTCTAGAGACA 360

OY 1435 GACAACTTAACCTCGTCCCGACAGAGAGACTTGATGAGG 1475
DB 361 GACAACTTAACCTCGTCCCGACAGAGAGACTTGATGAGG 401

RESULT 15
AI193544 405 bp mRNA linear EST 13-OCT-1998
LOCUS ge70e01.x1 Soares_fetal_lung_NbH19w Homo sapiens cDNA clone
DEFINITION IMAGE:1744344 3', mRNA sequence.
ACCESSION AI193544
VERSION AI193544.1 GI:3744753
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 399.
FEATURES
Source location/Qualifiers
1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744344"
/clone_lib="Soares_fetal_lung_NbH19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pRT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer.
15'-TGTTCACCAATCTGAAGTGGAGCGCGCCGAATTTTATTTTATTTT-3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbH19w. "
BASE COUNT 122 a 107 c 96 g 80 t
ORIGIN
Query Match 25.3%; Score 397; DB 9; Length 405;
Best Local Similarity 98.8%; Pred. No. 1.4e-44;
Matches 400; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 61 AAGAGTCCCGTCGGATCCGCGCCACACACCTGCTAGCCACCGCGCGCGCCCTC 120

```

```

QY 1195 AGTGGCCCTGGCCACACTCCAGAAAACGATCAGAGAAATATTTTACATG 1254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AGTGGCTCTGGGGGACACTCCAGAAAACGATCAGAGAAATATTTTACATG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1255 AAAAATAGAGAGAGCTATTTTGTACATTGTGTTAAAGAGACAAAACTGAAC 1314
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AAAAATAGAGAGAGCTATTTTGTACATTGTGTTAAAGAGACAAAACTGAAC 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1315 CAAAACTCTGGGGGAGGGGTGATTAAGATTTTATGTGACTGAACCCCGATGAC 1374
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CAAAACTCTGGGGGAGGGGTGATTAAGATTTTATGTGACTGAACCCCGATGAC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1375 AAAAGACTCAGCAAAAGGACTGTAGTCAACCCACAGGTGCTCTCTCTAGAAC 1434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AAAAGACTCAGCATAGGACTGTAGTCAACCCACAGGTGCTCTCTCTAGAAC 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1435 GACAACTCTAAACTGTCCCGAGAGAGACTTGATGAGGAAC 1479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 GACAACTCTAAACTGTCTCAGAGAGAGACTTGATGAGGAAC 405
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: April 26, 2003, 17:43:12
 Job time : 1617 secs

THIS PAGE BLANK (USPTO)